

**AMENDMENTS TO THE CLAIMS**

Please amend claims 30 and 35, as indicated below.

1-10. (Canceled)

11. (Original) A method of identifying from the genomic data of an individual organism a suitable therapy for at least one disease of the organism,

the method particularly serving to identify a relationship between, on a one hand, at least one therapy for at least one disease of an organism, and, on the other hand, genomic data of the organism in the form of two or more alleles and/or SNP pattern(s) of the organism

the method still more particularly serving to determine which of a large number of alleles as variously occur in the genomic data of a large number of individual organisms are, in actual fact, relevant, both individually and in combination, to certain biological and social variables of these organisms, including the efficacy of at least one therapy to at least one disease of these organisms,

the method comprising:

1) constructing a neural network suitable to map (i) genomic data in the form of two or more alleles and/or SNP patterns of

individual organisms as inputs to (ii) historical incidences of responses to therapies for diseases of the individual organisms as outputs; and

2) training the constructed neural network on numerous examples of (i) genomic data as corresponds to (ii) historical incidences of responses to therapies for the diseases of, a multiplicity of individual organisms so as to make a trained neural network that is fit, and that possesses a measure of goodness, to map (i) said genomic data to (ii) incidences of responses to therapies for the diseases of the organisms; and

3) exercising the trained constructed neural network in respect of a particular therapy for a particular disease, taken from among the therapies and the diseases to which the neural network was trained, in order to identify a relationship between the particular therapy and genomic data, in the form of two or more alleles, of the organisms.

12-13. (Canceled)

14. (Previously presented) The method according to claim 11 wherein the training is automated by computerized programmed operations using a genetic algorithm.

15. (Previously presented) The method according to claim 11 wherein the training is automated by computerized programmed operations using a genetic algorithm reduced in computational complexity by including the steps of:

grouping alleles and/or characteristic SNP patterns into families as are defined by (i) having similar expression patterns or (ii) being turned on and off by another gene, or (iii) both having similar expression patterns and being turned on and off by the same gene; and

starting training of the neural network with the genetic algorithm by using the families so created as single inputs to the neural network, the training with the genetic algorithm continuing repetitively until, families of greater and lessor significance being identified, it becomes computationally possible to train the neural network to genomic data consisting of individual alleles and/or characteristic SNP patterns;

wherein partitioning of all alleles and/or characteristic SNP patterns into families permits training of the neural network in a hierarchy of stages, first to the families and only then to the individual alleles and/or characteristic SNP patterns.

16-26. (Canceled)

27. (Previously presented) The method according to claim 11 that, at a time before the training of the constructed neural network on numerous examples further comprises:

obtaining, as a first portion of the numerous examples upon which the constructed neural network is trained, (i) genomic data in the form of alleles datums of types taken from a first group consisting essentially of

- entire gene families,
- specific alleles,
- specific base pair sequences,
- locations and types of introns, and
- nucleotide polymorphism,

plus at least one member of a second, environmental, group consisting essentially of

- diet type,
- home region,
- occupation,
- viral levels,
- peptide levels,
- blood plasma levels, and
- pharmacokinetic and pharmacodynamic parameters.

28. (Previously presented) The method according to claim 27

wherein the obtaining, as a first portion of the numerous examples upon which the neural network is trained, (i) genomic data in the form of alleles datums from a third, combination genetic and environmental, group consisting essentially of

ethnicity, and

race.

29. (Previously presented) A computerized method of identifying from the genomic data of an individual organism a suitable therapy for at least one disease of the organism, the method comprising:

constructing a neural network relating as inputs (i) genomic data in the form of two or more alleles and/or SNP patterns of individual organisms to outputs in the form of (ii) historical incidences of responses to therapies for diseases of the same individual organisms; and

training the neural network so constructed on numerous (i) genomic datums, as correspond to (ii) historical incidences of responses to therapies for the diseases, of a multiplicity of individual organisms;

therein making a trained neural network that is fit, and that possesses a measure of goodness, to map (i) said genomic data to (ii) incidences of responses to therapies for the diseases of the

organisms; and

exercising the trained constructed neural network in respect of a particular therapy for a particular disease, taken from among the therapies and the diseases to which the neural network was trained, in order to identify a relationship between a particular therapy and the genomic data, in the form of two or more alleles, of an individual organism;

wherein from the identified relationship it is determinable whether the particular therapy is suitable for the individual organism.

30. (Currently amended) A neural network residing on a computer and

suitable to map (i) genomic data in the form of two or more alleles and/or SNP patterns of individual organisms as inputs to (ii) historical incidences of responses to therapies for diseases of the individual organisms as outputs; and

trained on numerous examples of (i) genomic data as corresponds to (ii) historical incidences of responses to therapies for the diseases of, a multiplicity of individual organisms so as to be fit, and to possesses a measure of goodness, to map (i) said genomic data to (ii) incidences of responses to therapies for the diseases of the organisms;

wherein the trained neural network is exercisable in respect of a particular therapy for a particular disease, taken from among the therapies and the diseases to which the neural network was trained, in order to identify a relationship between the particular therapy and genomic data, in the form of two or more alleles, of the organisms.

31. (Previously presented) The trained neural network according to claim 30 trained by computerized programmed operations using a genetic algorithm.

32. (Previously presented) The trained neural network according to claim 30 trained by computerized programmed operations using a genetic algorithm is reduced in computational complexity by including the steps of:

grouping alleles and/or characteristic SNP patterns into families as are defined by (i) having similar expression patterns or (ii) being turned on and off by another gene, or (iii) both having similar expression patterns and being turned on and off by the same gene; and

starting training of the neural network with the genetic algorithm by using the families so created as single inputs to the neural network, the training with the genetic algorithm continuing

repetitively until, families of greater and lessor significance being identified, it becomes computationally possible to train the neural network to genomic data consisting of individual alleles and/or characteristic SNP patterns;

wherein partitioning of all alleles and/or characteristic SNP patterns into families permits training of the neural network in a hierarchy of stages, first to the families and only then to the individual alleles and/or characteristic SNP patterns.

33. (Previously presented) The trained neural network according to claim 30 that is trained on the numerous examples obtained, in a first portion, from (i) genomic data in the form of alleles datums of types taken from a first group consisting essentially of

entire gene families,

specific alleles,

specific base pair sequences,

locations and types of introns, and

nucleotide polymorphism,

plus at least one member of a second, environmental, group consisting essentially of

diet type,

home region,



occupation,  
viral levels,  
peptide levels,  
blood plasma levels, and  
pharmacokinetic and pharmacodynamic parameters.

34. (Previously presented) The trained neural network according to claim 33 that is trained on the numerous examples further obtained, still in the first portion, from (i) genomic data in the form of alleles datums of types taken from a third, combination genetic and environmental, group consisting essentially of  
ethnicity, and  
race.

35. (Currently amended) A neural network residing on a computer and functioning to identify from the genomic data of an individual organism a suitable therapy for at least one disease of the organism, the neural network  
relating as inputs (i) genomic data in the form of two or more alleles and/or SNP patterns of individual organisms to outputs in the form of (ii) historical incidences of responses to therapies for diseases of the same individual organisms; and

being trained on numerous (i) genomic datums, as correspond to (ii) historical incidences of responses to therapies for the diseases, of a multiplicity of individual organisms; and, by virtue of so relating and of being so ~~not~~ trained

being fit, meaning possessing a measure of goodness, to map (i) said genomic data to (ii) incidences of responses to therapies for the diseases of the organisms when exercised in respect of a particular therapy for a particular disease, taken from among the therapies and the diseases to which the training was directed, in order to identify a relationship between a particular therapy and the genomic data, in the form of two or more alleles, of an individual organism;

wherein from exercising of the trained neural network possessing the measure of goodness on the identified relationship it is determinable whether the particular therapy is suitable for the individual organism.